

RAW SEQUENCE LISTING DATE: 09/28/2000
 PATENT APPLICATION: US/09/662,784 TIME: 09:31:16

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\09282000\I662784.raw

SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: Bruce L. Rogers et al.i
8   (ii) TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
9         (TFRP) ISOLATED FROM HOUSE DUST AND USES THEREFOR
11  (iii) NUMBER OF SEQUENCES: 103
13  (iv) CORRESPONDENCE ADDRESS:
14        (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
15        (B) STREET: 28 State Street
16        (C) CITY: Boston
17        (D) STATE: Massachusetts
18        (E) COUNTRY: USA
19        (F) ZIP: 02109
21  (v) COMPUTER READABLE FORM:
22        (A) MEDIUM TYPE: Floppy disk
23        (B) COMPUTER: IBM PC compatible
24        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27  (vi) CURRENT APPLICATION DATA:
C--> 28        (A) APPLICATION NUMBER: US/09/662,784
C--> 29        (B) FILING DATE: 15-Sep-2000
31  (vii) PRIOR APPLICATION DATA:
32        (A) APPLICATION NUMBER: US 08/431,184
33        (B) FILING DATE: 27-APR-1995
36        (A) APPLICATION NUMBER: US 08/430,014
37        (B) FILING DATE: 27-APR-1995
40        (A) APPLICATION NUMBER: US 08/300,928
41        (B) FILING DATE: 02-SEPT-1994
43  (viii) ATTORNEY/AGENT INFORMATION:
44        (A) NAME: Amy E. Mandragouras
45        (B) REGISTRATION NUMBER: 36,207
46        (C) REFERENCE/DOCKET NUMBER: IMI-044DV3
48  (ix) TELECOMMUNICATION INFORMATION:
49        (A) TELEPHONE: (617)227-7400
50        (B) TELEFAX: (617)742-4214
53 (2) INFORMATION FOR SEQ ID NO: 1:
55   (i) SEQUENCE CHARACTERISTICS:
56        (A) LENGTH: 418 base pairs
57        (B) TYPE: nucleic acid
58        (C) STRANDEDNESS: single
59        (D) TOPOLOGY: linear
61   (ii) MOLECULE TYPE: cDNA
64   (ix) FEATURE:
65        (A) NAME/KEY: CDS
66        (B) LOCATION: 2..283
68   (ix) FEATURE:
69        (A) NAME/KEY: mat_peptide

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70      (B) LOCATION: 74..283
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 C TGC ATC ATG AAG GGG GCT CGT GTT CTC GTG CTT CTC TGG GCT GCC      46
76   Cys Ile Met Lys Gly Ala Arg Val Leu Val Leu Leu Trp Ala Ala
77   -24      -20      -15      -10
79 TTG CTC TTG ATC TGG GGT GGA AAT TGT GAA ATT TGC CCA GCC GTG AAG      94
80 Leu Leu Leu Ile Trp Gly Gly Asn Cys Glu Ile Cys Pro Ala Val Lys
81      -5      1      5
83 AGG GAT GTT GAC CTA TTC CTG ACG GGA ACC CCC GAC GAA TAT GTT GAG      142
84 Arg Asp Val Asp Leu Phe Leu Thr Gly Thr Pro Asp Glu Tyr Val Glu
85      10      15      20
87 CAA GTG GCA CAA TAC AAA GCA CTA CCT GTA GTA TTG GAA AAT GCC AGA      190
88 Gln Val Ala Gln Tyr Lys Ala Leu Pro Val Val Leu Glu Asn Ala Arg
89      25      30      35
91 ATA CTG AAG AAC TGC GTT GAT GCA AAA ATG ACA GAA GAG GAT AAG GAG      238
92 Ile Leu Lys Asn Cys Val Asp Ala Lys Met Thr Glu Glu Asp Lys Glu
93 40      45      50      55
95 AAT GCT CTC AGC TTG CTG GAC AAA ATA TAC ACA AGT CCT CTG TGT      283
96 Asn Ala Leu Ser Leu Leu Asp Lys Ile Tyr Thr Ser Pro Leu Cys
97      60      65      70
99 TAAAGGAGCC ATCACTGCCA GGAGCCCTAA GGAAGCCACT GAACTGATCA CTAAGTAGTC      343
101 TCAGCAGCCT GCCATGTCCA GGTGTCTTAC TAGAGGATTC CAGCAATAAA AGCCTGGCAA      403
103 TTCAACAACA AAAAAA      418
106 (2) INFORMATION FOR SEQ ID NO: 2:
108   (i) SEQUENCE CHARACTERISTICS:
109       (A) LENGTH: 94 amino acids
110       (B) TYPE: amino acid
111       (D) TOPOLOGY: linear
113   (ii) MOLECULE TYPE: protein
115   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
117 Cys Ile Met Lys Gly Ala Arg Val Leu Val Leu Leu Trp Ala Ala Leu
118 -24      -20      -15      -10
120 Leu Leu Ile Trp Gly Gly Asn Cys Glu Ile Cys Pro Ala Val Lys Arg
121      -5      1      5
123 Asp Val Asp Leu Phe Leu Thr Gly Thr Pro Asp Glu Tyr Val Glu Gln
124      10      15      20
126 Val Ala Gln Tyr Lys Ala Leu Pro Val Val Leu Glu Asn Ala Arg Ile
127 25      30      35      40
129 Leu Lys Asn Cys Val Asp Ala Lys Met Thr Glu Glu Asp Lys Glu Asn
130      45      50      55
132 Ala Leu Ser Leu Leu Asp Lys Ile Tyr Thr Ser Pro Leu Cys
133      60      65      70
136 (2) INFORMATION FOR SEQ ID NO: 3:
138   (i) SEQUENCE CHARACTERISTICS:
139       (A) LENGTH: 420 base pairs
140       (B) TYPE: nucleic acid
141       (C) STRANDEDNESS: single
142       (D) TOPOLOGY: linear
144   (ii) MOLECULE TYPE: cDNA

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147      (ix) FEATURE:
148          (A) NAME/KEY: CDS
149          (B) LOCATION: 2..289
151      (ix) FEATURE:
152          (A) NAME/KEY: mat_peptide
153          (B) LOCATION: 80..289
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
158 G  GCC TGG CGG TGC TCC TGG AAA AGG ATG TTA GAC GCA GCC CTC CCA      46
159 Ala Trp Arg Cys Ser Trp Lys Arg Met Leu Asp Ala Ala Leu Pro
160 -26 -25 -20 -15
162 CCC TGC CCT ACT GTT GCG GCC ACA GCA GAT TGT GAA ATT TGC CCA GCC      94
163 Pro Cys Pro Thr Val Ala Ala Thr Ala Asp Cys Glu Ile Cys Pro Ala
164 -10 -5 1 5
166 GTG AAG AGG GAT GTT GAC CTA TTC CTG ACG GGA ACC CCC GAC GAA TAT      142
167 Val Lys Arg Asp Val Asp Leu Phe Leu Thr Gly Thr Pro Asp Glu Tyr
168 10 15 20
170 GTT GAG CAA GTG GCA CAA TAC AAA GCA CTA CCT GTA GTA TTG GAA AAT      190
171 Val Glu Gln Val Ala Gln Tyr Lys Ala Leu Pro Val Val Leu Glu Asn
172 25 30 35
174 GCC AGA ATA CTG AAG AAC TGC GTT GAT GCA AAA ATG ACA GAA GAG GAT      238
175 Ala Arg Ile Leu Lys Asn Cys Val Asp Ala Lys Met Thr Glu Glu Asp
176 40 45 50
178 AAG GAG AAT GCT CTC AGC TTG CTG GAC AAA ATA TAC ACA AGT CCT CTG      286
179 Lys Glu Asn Ala Leu Ser Leu Leu Asp Lys Ile Tyr Thr Ser Pro Leu
180 55 60 65
182 TGT TAAAGGAGCC ATCACTGCCA GGAGCCCTAA GGAAGCCACT GAACTGATCA      339
183 Cys
184 70
186 CTAAGTAGTC TCAGCAGCCT GCCATGTCCA GGTGTCTTAC TAGAGGATTC CAGCAATAAA      399
188 AGCCTTGCAA TTCAAAACAAA A      420
191 (2) INFORMATION FOR SEQ ID NO: 4:
193      (i) SEQUENCE CHARACTERISTICS:
194          (A) LENGTH: 96 amino acids
195          (B) TYPE: amino acid
196          (D) TOPOLOGY: linear
198      (ii) MOLECULE TYPE: protein
200      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
202 Ala Trp Arg Cys Ser Trp Lys Arg Met Leu Asp Ala Ala Leu Pro Pro
203 -26 -25 -20 -15
205 Cys Pro Thr Val Ala Ala Thr Ala Asp Cys Glu Ile Cys Pro Ala Val
206 -10 -5 1 5
208 Lys Arg Asp Val Asp Leu Phe Leu Thr Gly Thr Pro Asp Glu Tyr Val
209 10 15 20
211 Glu Gln Val Ala Gln Tyr Lys Ala Leu Pro Val Val Leu Glu Asn Ala
212 25 30 35
214 Arg Ile Leu Lys Asn Cys Val Asp Ala Lys Met Thr Glu Glu Asp Lys
215 40 45 50
217 Glu Asn Ala Leu Ser Leu Leu Asp Lys Ile Tyr Thr Ser Pro Leu Cys
218 55 60 65 70

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221 (2) INFORMATION FOR SEQ ID NO: 5:
223   (i) SEQUENCE CHARACTERISTICS:
224       (A) LENGTH: 476 base pairs
225       (B) TYPE: nucleic acid
226       (C) STRANDEDNESS: single
227       (D) TOPOLOGY: linear
229   (ii) MOLECULE TYPE: cDNA
232   (ix) FEATURE:
233       (A) NAME/KEY: CDS
234       (B) LOCATION: 2..334
236   (ix) FEATURE:
237       (A) NAME/KEY: mat_peptide
238       (B) LOCATION: 59..334
241   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
243 T GAC ACG ATG AGG GGG GCA CTG CTT GTG CTG GCA TTG CTG GTG ACC      46
244   Asp Thr Met Arg Gly Ala Leu Leu Val Leu Ala Leu Leu Val Thr
245   -19          -15          -10          -5
247 CAA GCG CTG GGC GTC AAG ATG GCG GAA ACT TGC CCC ATT TTT TAT GAC      94
248   Gln Ala Leu Gly Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp
249   -1          1          5          10
251 GTC TTT TTT GCG GTG GCC AAT GGA AAT GAA TTA CTG TTG GAC TTG TCC      142
252   Val Phe Phe Ala Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser
253   15          20          25
255 CTC ACA AAA GTC AAT GCT ACT GAA CCA GAG AGA ACA GCC ATG AAA AAA      190
256   Leu Thr Lys Val Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys
257   30          35          40
259 ATC CAG GAT TGC TAC GTG GAG AAC GGA CTC ATA TCC AGG GTC TTG GAT      238
260   Ile Gln Asp Cys Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp
261   45          50          55          60
263 GGA CTA GTC ATG ACA ACC ATC AGC TCC AGC AAA GAT TGC ATG GGT GAA      286
264   Gly Leu Val Met Thr Thr Ile Ser Ser Ser Lys Asp Cys Met Gly Glu
265   65          70          75
267 GCA GTT CAG AAC ACC GTA GAA GAT CTC AAG CTG AAC ACT TTG GGG AGA      334
268   Ala Val Gln Asn Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg
269   80          85          90
271 TGAATCTTTT CCCTGATGC CCCTTCTGAG CCCCATCCTC CTGCCCTGTT CTTTACACCT      394
273 AAAGCTGGAA TCCAGACACC TGTCCTCACC TAATTCACCTC TCAATCAGGC TGACTAGAAT      454
275 AAAATAACTG CATCTTAAAA AA
275 AAAATAACTG CATCTTAAAA AA      476
278 (2) INFORMATION FOR SEQ ID NO: 6:
280   (i) SEQUENCE CHARACTERISTICS:
281       (A) LENGTH: 111 amino acids
282       (B) TYPE: amino acid
283       (D) TOPOLOGY: linear
285   (ii) MOLECULE TYPE: protein
287   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
289 Asp Thr Met Arg Gly Ala Leu Leu Val Leu Ala Leu Leu Val Thr Gln
290   -19          -15          -10          -5
292 Ala Leu Gly Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp Val
293   1          5          10

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295 Phe Phe Ala Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser Leu
296      15      20      25
298 Thr Lys Val Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys Ile
299      30      35      40      45
301 Gln Asp Cys Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp Gly
302      50      55      60
304 Leu Val Met Thr Thr Ile Ser Ser Lys Asp Cys Met Gly Glu Ala
305      65      70      75
307 Val Gln Asn Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg
308      80      85      90
311 (2) INFORMATION FOR SEQ ID NO: 7:
313   (i) SEQUENCE CHARACTERISTICS:
314       (A) LENGTH: 469 base pairs
315       (B) TYPE: nucleic acid
316       (C) STRANDEDNESS: single
317       (D) TOPOLOGY: linear
319   (ii) MOLECULE TYPE: cDNA
322   (ix) FEATURE:
323       (A) NAME/KEY: CDS
324       (B) LOCATION: 1..327
326   (ix) FEATURE:
327       (A) NAME/KEY: mat_peptide
328       (B) LOCATION: 59..327
331   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
333 GAC ACG ATG AGG GGG GCA CTG CTT GTG CTG GCA TTG CTG GTG ACC CAA      48
334 Asp Thr Met Arg Gly Ala Leu Leu Val Leu Ala Leu Leu Val Thr Gln
335 -19 -15 -10 -5
337 GCG CTG GGC GTC AAG ATG GCG GAG ACG TGC CCC ATT TTT TAT GAC GTC      96
338 Ala Leu Gly Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp Val
339      1      5      10
341 TTT TTT GCG GTG GCC AAT GGA AAT GAA TTA CTG TTG GAC TTG TCC CTC      144
342 Phe Phe Ala Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser Leu
343      15      20      25
345 ACA AAA GTC AAT GCT ACT GAA CCA GAG AGA ACA GCC ATG AAA AAA ATC      192
346 Thr Lys Val Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys Ile
347      30      35      40      45
349 CAG GAT TGC TAC GTG GAG AAC GGA CTC ATA TCC AGG GTC TTG GAT GGA      240
350 Gln Asp Cys Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp Gly
351      50      55      60
353 CTA GTC ATG ATA GCC ATC AAC GAA TAT TGC ATG GGT GAA GCA GTT CAG      288
354 Leu Val Met Ile Ala Ile Asn Glu Tyr Cys Met Gly Glu Ala Val Gln
355      65      70      75
357 AAC ACC GTA GAA GAT CTC AAG CTG AAC ACT TTG GGG AGA TGAATCTTTG      337
358 Asn Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg
359      80      85      90
361 CCACTGATGC CCCTTCTGAG CCCCATCCTC CTGTCCTGTT CTTTACACCT AAAGCTGGAA      397
363 TCCAGACACC TGCTCTCACC TAATTCACCT TCAATCAGGC TGACTAGAAT AAAATAACTG      457
365 CATCTTAAAA AA      469
368 (2) INFORMATION FOR SEQ ID NO: 8:

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PATENT APPLICATION: US/09/662,784 TIME: 09:31:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09282000\I662784.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:675 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:680 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:685 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:690 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:695 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:700 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16